

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 35, line 5 as follows:

A second example involves the human reference sequence for spermidine/spermine N1-acetyltransferase (SAT) mRNA. The human reference sequence for spermidine/spermine N1-acetyltransferase (SAT) mRNA (~~see <http://www3.ncbi.nlm.nih.gov/LocusLink/LocRpt.cgi?l=6303> for details~~) includes a portion of the mRNA polyA tail at its 3'-end. The most 3' probe to this gene on the tiling array of this example has the sequence

TTGATTCTTTTTTAATAAACTACTCTTTGATTAAAAA
AAA, SEQ ID 29

which includes both a 3'-run of 27 A's and a low complexity 5'-end that is T-rich. The log expression ratio results from differential expression and self-comparison experiments on this gene are shown in Figure 15. From Figure 15, it is clear that the log expression ratios measured in self-comparison experiments are near zero, as expected. In contrast, all but the 3'-most probe measure a nearly 4-fold over-expression of the gene in HeLa, versus K562; the log expression ratio reverses sign when the dye labels are swapped, as expected. However, the 3'-most probe, which was identified by Repeat Masker as containing unacceptably high levels of low complexity sequence, reports a log ratio of zero. These results indicate that this low complexity probe is another example of a probe that measures the average total signal in each dye label channel. Thus, the probe can be used to normalize 2-color microarray data.